

In the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

1. (Currently Amended) A crystal comprising of a polypeptide having the amino acid sequence of residues 29-766 of SEQ ID NO: 2 dipeptidyl peptidase IV wherein the crystal diffracts x-rays for the determination of the atomic coordinates of the polypeptide at a resolution of 3 Å or less, having characteristics sufficient to ensure a resolution capable of analyzing its three-dimensional structure up to the side chain level by X-ray crystallographic structural analysis.
2. (Cancelled)
3. (Currently Amended) The A crystal comprising a polypeptide having the amino acid sequence of residues 33-766 of SEQ ID NO: 2 wherein the crystal diffracts x-rays for the determination of the atomic coordinates of the polypeptide at a resolution of 3 Å or less, according to claim 1 or 2, wherein the dipeptidyl peptidase IV is a polypeptide having an amino acid sequence in which a transmembrane region is deleted from the amino acid sequence of SEQ ID NO: 2, and a tag peptide is optionally added to a C-terminal side or N-terminal side thereof.
4. (Currently Amended) The crystal according to claim 1 or 3 any one of claims 1 to 3, wherein the crystal has a space group of P2₁2₁2₁, and a lattice constant of the unit cell of |a| = 118.0 ± 5.0 Å, |b| = 125.9 ± 5.0 Å, |c| = 136.8 ± 5.0 Å, and $\alpha = \beta = \gamma = 90^\circ$, and is orthorhombic.
5. (Currently Amended) The crystal according to claim 1 or 3 any one of claims 1 to 4, wherein the crystal has the structural coordinates shown in Figure 4.

6. (Currently Amended) The crystal according to claim 1 or 3 any one of claims 1 to 4, wherein the crystal has a structural coordinates different from the structural coordinates as shown in Figure 4 via fluctuation of a protein.

7-24. (Cancelled)

25. (New) The crystal according to claim 1 or 3, wherein the polypeptide further comprises a polyhistidine tag.

26. (New) The crystal according to claim 1 or 3 wherein the crystal diffracts x-rays for the determination of the atomic coordinates of the polypeptide at a resolution of 2.8 Å or less.

27. (New) The crystal according to claim 1 or 3 wherein the crystal diffracts x-rays for the determination of the atomic coordinates of the polypeptide at a resolution of 2.6 Å or less.

28. (New) The crystal according to claim 1 or 3, wherein amino acid residues Ser 630, Asp 708 and His 740 of SEQ ID NO:2 have the structural coordinates shown in Figure 4.